Application of international health regulations in the Singapore pandemic influenza experience

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Background: The global spread of novel influenza A (H1N1-2009) constituted a public health emergency of international concern (PHEIC). Singapore's defense against this pandemic strain comprised public health measures in compliance with WHO's International Health Regulations (IHR), 2005. We report herein on the epidemiology and control of the first 350 cases notified in May-Jun 2009.

Methods: We investigated into the first 350 laboratory-confirmed cases of novel influenza A (H1N1-2009) identified from the healthcare institutions between 27 May and 25 Jun 2009.

Epidemiological details of these cases were retrieved and analysed. Contact tracing and active case finding were also instituted for each reported case, and relevant particulars including flight information provided to WHO and overseas counterparts.

Results: The first 350 novel influenza A (H1N1-2009) cases comprised 221(63%) imported cases, 124 (35%) locally acquired cases and 4(2%) cases with unknown source. The imported cases consisted of three waves involving the US, Australia and Southeast Asia. In the first wave, 11 (69%) of the 16 imported cases had visited the USA within seven days prior to their onset of illness between 25 May and 4 Jun 2009. In the second wave, 20 (74%) of the 27 imported cases between 5 Jun and 12 Jun had traveled to Melbourne, Australia. In the third wave, 90 (50.6%) of the 178 imported cases between 13 Jun and 25 Jun were acquired from intra-regional travel in Southeast Asia. Specifically, 49 cases were from the Philippines and 40 (82%) of them had traveled to Manila. A total of 667 communications were effected through the IHR mechanism, majority within 24 hours of disease notification.

Conclusion: Singapore experienced an unprecedented level of international cooperation for surveillance and response to this novel Influenza A (H1N1-2009) pandemic. Through the timely sharing and open reporting of major public health events, we established a network of collaboration which facilitated not only notification of confirmed cases, but also bilateral communications in a manner that was rational, predictable and productive. The IHR mechanism has served as an effective channel to engage in regional cooperation concerning disease surveillance and data sharing.

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Models and data for determining transmission routes

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Background: Multiple modes of transmission are possible for respiratory infections. For example influenza might be spread via small droplet aerosols that get down into the between individuals or contaminate hands or fomites that carry infectious agent to a new host. Methodology to study the frequency of different transmission modes and the role that they play in amplifying or disseminating transmission throughout populations has been lacking.

Methods: Environmental Infection Transmission System Models were formulated that range from highly abstract to highly detailed. These models follow the infectious agent out of one person, through the environment, to another individual, and then through the immune elements that could eliminate them until they start an infection. These models are analyzed mathematically and numerically. Then they are run with different hypothetical types of data in order to determine what types of data would be most helpful in determining what modes of transmission are acting in the real world.

Results: The abstract models show that different modes of transmission will be expected to have different relationships that constrain the number of individuals that can be infected via that mode. The more detailed models show that for influenza, different routes of transmission will dominate under different conditions. The framework for determining infection mode from real world data involves relating a hierarchy of data types to a hierarchy of model types in a manner that assesses the robustness of inferences about modes of transmission to realistically relaxing extreme simplifying assumptions in the models and then finding a reasonable data set that can estimate model parameters.

Conclusion: Data from a single venue on who gets infected given different levels of environmental contamination and their exposure to that contamination will be very difficult to gather in a manner that allows for definitive conclusions about transmission mode. Data on genetic variation patterns of pathogens in different environments where different modes of transmission might dominate could be more productive.

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Epidemiological transition in Venezuela: Relationships between infectious diarrheas, ischemic heart diseases and transportation accidents mortalities and the human development index (HDI) in Venezuela, 2005-2007

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Background: The objective of this study is to describe potential relationships between the Human Development Index (HDI) and its components and the mortality due to infectious diarrheas (ID), ischemic heart diseases (IHD) and transportation accidents (TA) in the 23 States and DC of Venezuela between 2005-2007 as a reflect of epidemiological transition in the country.

Methods: Socioeconomical data (classified according the WB) was obtained from the National Institute of Statistics, including the HDI and its components life expectancy, literacy, education, standard of living, and GDP per capita; and the epidemiological data (mean rates) from the Ministry